Review Article

A REVIEW ON GENETIC DIVERSITY OF WILD PLANTS BY USING DIFFERENT GENETIC MARKERS

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Abstract

Biodiversity is the variation of life at all levels of biological organization. One of the important components of biological diversity is the genetic diversity. Genetic diversity refers to the variation of genes or entire genome within and between populations of organisms. Keeping in view the significance of genetic diversity in wild plants, some research articles based on important wild plant genera and species of angiosperms including few rare, threatened, endemic, medicinal and economically important from different regions of the world are reviewed. The genetic diversity of plant species depends on different factors i.e. ecological, geographical, breeding system & anthropogenic effects. High genetic diversity is observed at species level even in small sized population by using AFLP, SSR, & ISSR genetic markers.

Keywords: Genetic Diversity; Genetic Structure; Genetic Markers; Species diversity; wild plants

Abbreviations:

AFLP Amplified fragment length polymorphism
DArT Diversity Arrays technology
ISSR Inter simple sequence repeat
RAPD Rapid amplification polymorphism of DNA
RFLP Restriction fragment length polymorphism
SSR Simple sequence repeat

Introduction

Biodiversity is the variation of life at all levels of biological organizations [1]. Biodiversity may also be defined as the "totality of genes, species, and ecosystems of a region" [2].

Genetic diversity is one of the important constituent of biological diversity. Research on biological diversity explains the species diversity within diverse ecosystems can help exploring genetic diversity and genetic structure of a specific population can provide a molecular basis for understanding its biological characteristics, phylogeny and adaptive potential. DNA markers are considered to be the most suitable means for estimating genetic diversity because of their abundant polymorphism and the fact that they are independent of environmental conditions [3-5].

Genetic Structure

Reproductive characters and population history mainly determine the genetic diversity in

plant populations [6-7]. The influence of the plant's mating system affect the Plant reproductive characters and population genetic structure [8]. Mostly inbreeding species have homozygosity and lesser genetic diversity within populations and higher genetic differentiation among populations compared without crossing species [8].

It reveals to a certain degree that the relative rates of inbreeding and out crossing in species are relevant to the genetic diversity within and among populations. Population history, including the phylogeny and biogeography of a species as well as fluctuations in the number of populations may also play a significant role in the formation of its current genetic composition [6]. Existing biogeographic patterns of genetic diversity are determined by historical patterns of gene flow among populations [9-11]. Thus, the genetic structure of a species can explain its evolutionary history [12].

Connections between species diversity and genetic Diversity

Species diversity and genetic diversity can be defined and measured in a number of different ways.

Species diversity is most often measured as species richness, the number of species in a given locality. In studies that experimentally manipulate species diversity [13] (reviewed by Loreau *et al.*, 2001) mostly species richness varied among treatments. Many studies of species diversity integrate information about the relative abundances of species in a region, with higher diversity indicated by a more even distribution of abundance among species higher evenness [14].

In population genetics and community ecology species diversity and genetic diversity are important constituents along with ecological diversity. Species diversity within communities and genetic diversity within populations are thought to be different in space or time because of their habitat that influence the two levels of diversity by similar processes, or because of direct effects of one level of diversity on the other by means of several different mechanisms. A species diversity–genetic diversity relationship is supported by a number of theories and experimental studies, and several modern studies support this connection. Emphasizing on all possible associations between these two domains help in better understanding and synthesis at the ecological and phylogenetic aspects of systematics and biodiversity research at the levels of genes and species [15].

Genetic Markers

A genetic marker is a sequence of DNA or a gene, present on a chromosome [16-17]. Markers make it possible to detect differences between individuals by showing polymorphism, and therefore detecting genetic differences between individual organisms or species [16].

DNA markers are used in many different areas, such as genetic mapping, finding mutant genes which are connected to hereditary diseases, paternal tests, individual identification, epidemiology and food safety, population history, population studies, etc [18].

The studies may use RFLPs, RAPDs, AFLPs or SSRs. It is important to understand the properties of different markers that will reveal different aspects of genetic diversity [19].

Polyploidy, the presence of more than two sets of chromosomes within an organism, is a pervasive phenomenon in flowering plants [20-22].

Polyploids are typically grouped into autopolyploids (produced by multiplication of a single genome) and allopolyploids (combination of two or more divergent genomes). In a successful allopolyploid, two parental genomes must function within a common cytoplasm, which may be associated with numerous genetic, epigenetic, and transcriptomic changes [23-25].

Diversity Arrays Technology (DArT)

Diversity Arrays Technology (DArT) can detect and type DNA variation at several hundred genomic loci in parallel without relying on sequence information. It can be effectively applied to genetic mapping and diversity analyses of barley, a species with a 5,000-Mbp genome [26].

Herbarium specimens as a source of DNA for AFLP fingerprinting

Herbarium collections are a valuable source of genetic information. Even though the DNA obtained from the specimens is often highly fragmented and present in small quantities, it has been successfully used particularly for DNA sequencing and microsatellite analysis. The present study shows that the quality is often sufficient for use also for AFLPs. With this technique, a considerable number of DNA fragments with unknown sequence from the entire genome of the plant are amplified, often with the purpose of phylogeographic studies or analyses of interrelationships of closely related species [27].

Microsatellites or simple sequence repeats (SSRs)

These are short (1–8 bp) repeat motifs usually associated with a high level of frequency of length polymorphism. SSR markers are one of the best choices for genetic research and breeding with the advantages of their stability, PCR-based and relatively low cost. SSR markers can be developed experimentally [28].

Inter-simple sequence repeats (ISSRs)

These are regions found between microsatellite repeats, ISSR have been used since 1994 for a wide range of organisms [5] in DNA fingerprinting, diversity analysis and genome mapping [29-30]. The advantages of using ISSR are that it is quick, easy to apply, highly reproducible and polymorphous. The major significance is that no prior information about genomic sequence is required [29].

Table-1: Reported wild plant species for genetic diversity from different regions of the world.

Plant Name	Country	References
<i>Rheumofficinale</i> Baill.,	China	Wang <i>et al.</i> , 2012 [31]
<i>Rhodiola rosea</i> L.	Sweden/Greenland/Faroe Islands	Kylin, M. 2010 [32]
<i>Saruma henryi</i> Oliv.	China	Zhou <i>et al.</i> , 2012 [33]
<i>Galium</i> sp L.	North Eastern Europe	Cieślak & Szlag 2010. [34]
<i>Caragana</i> sp Fabr.	China	Yang <i>et al.</i> , 2012. [35]
<i>Malus</i> sp L.	China	Zhang <i>et al.</i> , 2011. [36]

Conclusion

Study and analysis of genetic diversity by using different genetic markers resulted in the form of polymorphic bands, Shannon's information index and other tools, help in understanding the genetic variability of species within and between populations. Genetic diversity of endemic, narrow endemic and endangered species can be conserved by ex-situ and in-situ conservation strategies. Germplasm preservation, seed bank, gene bank management and sustainable development can also be accomplished by appropriate utilization of genetic diversity.

There is a dire need for all those interested in plant genetic resources conservation, needs better understanding of genetic diversity at all levels.

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Table-1: : Parts used for DNA extraction to study genetic diversity and Consequences of reported wild plants

Plant Name	Parts used	Marker s used	Results	Refere nces
<i>Rheum officinale</i> Baill.	Dried roots and rhizomes	ISSR	Results revealed high genetic diversity at spp.level. PPB obtained were 95.24%	Wang <i>et al.</i> , [31] 2012
<i>Rhodiola rosea</i> L.	Leaves	SSR & ISSR	An average PPB for ISSR were 75.68% Highest in Greenland as compare to other study areas.	Kylin, M. [32] 2010
<i>Saruma henryi</i> Oliv.	Leaves	SSR	High genetic diversity at spp. Level is being observed.	Zhou <i>et al.</i> , [33] 2012.
<i>Galium</i> sp L.	Leaves of young plants	AFLP	Results indicate high level of genetic variation in all 3species studied, despite of the small area occupied and low population.	Cieśla k & Szlag 2010. [34]
<i>Caragana</i> sp Fabr.	Fresh leaves	ISSR	Results of genetic diversity of eight Caragna spp. by using ISSR markers helped understanding high genetic diversity of all spp. Studied with max. PPB i.e. 100%.	Yang <i>et al.</i> , 2012. [35]
<i>Malus</i> sp L.	Leaf Tissues	SSR	29 Malus accessions were analysed resulting in 62.5% unique alleles Indicating high genetic diversity can be used by horticulturist and plant breeders.	Zhang <i>et al.</i> , 2011. [36]

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